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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.76512 Seconds

(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-17
Perfect score: 606
Sequence: 1 MOMWATFOQKHIIINTPIICN.....ICVCKENQYVHFAGIGRCP 111

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	585.5	96.6	111	1	RNPO_RANCA
2	449	74.1	111	1	LECS_RANCA
3	368	60.7	111	1	RNPL_RANCA
4	271.5	44.8	104	1	RN30_RANPI
5	148.5	24.5	145	1	ANG3_MOUSE
6	143.5	23.7	145	1	ANGR_MOUSE
7	129.5	21.4	124	1	RNP_BALAC
8	129.5	21.4	145	1	ANGI_MOUSE
9	127.5	21.0	167	1	RNBR_BOVIN
10	126.5	20.9	124	1	RNP_PIG
11	125.5	20.7	119	1	RNP_IGUG
12	122.5	20.2	151	1	RNBR_BOVIN
13	121.5	20.0	123	1	ANG2_BOVIN
14	121.5	20.0	141	1	RNBR_GIRCA
15	121.5	20.0	151	1	RNBR_AXIPC
16	119	19.6	146	1	ANGI_SAISC
17	118	19.5	146	1	ANGI_MIOFA
18	117.5	19.4	143	1	RNBR_SHEEP
19	116.5	19.2	124	1	RNP_ANTAM
20	116.5	19.2	146	1	ANGI_CERAE
21	116	19.1	122	1	RNP_MACRU
22	114.5	18.9	128	1	RNP_MYOCO
23	114.5	18.9	149	1	RNP_MOUSE
24	114	18.8	146	1	ANGI_AOTTR
25	114	18.8	147	1	ANGI_PONRY
26	113.5	18.7	123	1	ANGI_PIG
27	112.5	18.6	128	1	RNPE_CAYVO
28	112	18.5	146	1	ANGI_SAGOE
29	111.5	18.4	128	1	RNP_HORSE
30	110.5	18.2	124	1	RNP_CAMDR
31	110.5	18.2	128	1	RNP_CROGU
32	109.5	18.1	146	1	ANGI_MACMU
33	108	17.8	148	1	ANGI_BOVIN

34	107.5	17.7	124	1	RNP_RANCA	P00666 ranganfer ta
35	107.5	17.7	146	1	ANGI_PAPHA	O8w664 papio hamad
36	107	17.7	147	1	ANGI_HUMAN	P03950 homo sapien
37	107	17.7	147	1	ANGI_PANTR	O8w664 pan troglod
38	106.5	17.6	124	1	RNP_CAPCA	P00664 capreolus c
39	106.5	17.6	124	1	RNP_GIRCA	O91jhl giraffa cam
40	106.5	17.6	148	1	RNLA_MOUSE	O91jhl mus musculu
41	106	17.5	125	1	ANGI_RABIT	P31347 oryctolagus
42	105.5	17.4	130	1	RNP_CRILLO	P24717 citreulius
43	105.5	17.4	147	1	RNLA_RAT	O55004 rattus norv
44	105.5	17.4	149	1	RNP_ACOCA	O9wtls acowys calh
45	104.5	17.2	124	1	RNP_AEPME	P07847 aepyceros m

ALIGNMENTS

RESULT 1	ID	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).				
OS	Rana catesbeiana (Bull. frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_TaxID=8400;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Egg;				
RA	MEDLINE=87299649; PubMed=3304421;				
RA	Tilani K., Takio K., Kawada M., Nitta K., Sakakibara F., Kawachi H.,				
RA	Takayanagi G., Hakomori S.;				
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana				
RT	catesbeiana) eggs.";				
RL	Biochemistry 26:2189-2194(1987).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.				
RC	MEDLINE=92220613; PubMed=1373237;				
RA	Liao Y.-D.;				
RA	"A pyrimidine-guanine sequence-specific ribonuclease from Rana				
RT	catesbeiana (bullfrog) oocytes.";				
RL	Nucleic Acids Res. 20:1371-1377(1992).				
RN	[3]				
RP	CHARACTERIZATION.				
RC	TISSUE=Egg;				
RA	MEDLINE=93192604; PubMed=8448385;				
RA	Nitta K., Oyama F., Sekiguchi K., Kawachi H.,				
RT	Takayanagi Y., Hakomori S., Tilani K.;				
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana				
RL	catesbeiana eggs.";				
RL	Glycobiology 3:37-45(1993).				
RP	[4]				
RP	STRUCTURE BY NMR.				
RA	MEDLINE=98437383; PubMed=9761686;				
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;				
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes				
RT	of Rana catesbeiana (bullfrog).";				
RL	J. Mol. Biol. 283:231-244(1998).				
CC	- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE				
CC	RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)				
CC	AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS				
CC	MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG				
CC	EMBRYO. THIS LECTIN AGGLOUTINATES VARIOUS ANIMAL CELLS, INCLUDING				
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND				
CC	HUMAN ORIGIN.				
CC	- SUBUNIT: MONOMER.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PIR: A27121; A27121.				

DR PDB: 1BC4: 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA. 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease; Stalk acid; Lectin; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;

Query Match 96.6%; Score 585.5; DB 1; Length 111;
 Best Local Similarity 98.2%; Pred. No. 6.1e-57;
 Matches 109; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 2 ONMAFFQOKHIINPIL-CNTIMDNNTIYVGQCKRVTFITSSATVKAICTGVINMN 60
 DB 1 ONMAFFQOKHIINPILNCNTIMDNNTIYVGQCKRVTFITSSATVKAICTGVINMN 60
 OY 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVGCENQYVHFAGIGRC 111
 DB 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVGCENQYVHFAGIGRC 111

RESULT 2
 LEC5_RANJA STANDARD: PRT; 111 AA.
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stalk acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese redbellied frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE-Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamiya Y., Oyama F., Sakakibara F., Nitta K., Kawachi H.,
 Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 eggs";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSSP: P11916; 1BC4.
 DR PIR: JX0120; JX0120.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA. 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 KW HydroLase: Nuclease; Endonuclease; Stalk acid; Lectin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 93 97

FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 74.1%; Score 449; DB 1; Length 111;
 Best Local Similarity 77.3%; Pred. No. 4.2e-42;
 Matches 86; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

OY 2 ONMAFFQOKHIINPIL-CNTIMDNNTIYVGQCKRVTFITSSATVKAICTGVINMN 59
 DB 1 ONMAFFQOKHIINPILNCNTIMDNNTIYVGQCKRVTFITSSATVKAICTGVINMN 60
 OY 60 VLSSTRFQNLNCTRTSITPRCPYSSRTETNYICVGCENQYVHFAGIGRC 110
 DB 61 VLSSTRFQNLNCTRTSITPRCPYSSRTETNYICVGCENQYVHFAGIGRC 111

RESULT 3
 RNP5_RANCA STANDARD: PRT; 111 AA.
 ID RNP5_RANCA
 AC P14626;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, Liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
 liver";
 RL J. Biochem. 106:729-735(1989).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA. 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 KW HydroLase: Nuclease; Endonuclease.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 104 104
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10768 CRC64;

Query Match 60.7%; Score 368; DB 1; Length 111;
 Best Local Similarity 64.9%; Pred. No. 2.7e-33;
 Matches 72; Conservative 9; Mismatches 28; Indels 2; Gaps 2;

OY 2 ONMAFFQOKHIINPIL-CNTIMDNNTIYVGQCKRVTFITSSATVKAICTGVINMN 59
 DB 1 ONMAFFQOKHIINPILNCNTIMDNNTIYVGQCKRVTFITSSATVKAICTGVINMN 60
 OY 60 VLSSTRFQNLNCTRTSITPRCPYSSRTETNYICVGCENQYVHFAGIGRC 110
 DB 61 ELSTSTRFQNLNCTRTSITPRCPYSSRTETNYICVGCENQYVHFAGIGRC 111

RESULT 4
 RN30_RANPI STANDARD: PRT: 104 AA.
 AC P22069:
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE P-30 protein (EC 3.1.27.-) (Onconase).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RC SEQUENCE.
 RP Tissue=Embryo;
 RX MEDLINE=91093131; PubMed=1985896;
 RA Ardelt W., Mikulski S.M., Shogen K.;
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
 oocytes and early embryos. Homology to pancreatic ribonucleases.";
 RL J. Biol. Chem. 266:245-251(1991).
 RN [2]
 RC 3D-STRUCTURE MODELING.
 RX MEDLINE=93066156; PubMed=1438177;
 RA Mosmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
 James M.N.G.;
 RT "Comparative molecular modeling and crystallization of P-30 protein:
 a novel antitumor protein of Rana pipiens oocytes and early
 embryos.";
 RL Proteins 14:392-400(1992).
 RN [3]
 RC X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=94166079; PubMed=8120892;
 RA Mosmann S.C., Ardelt W., James M.N.G.;
 RT "Refined 1.7 A x-ray crystallographic structure of P-30 protein, an
 amphibian ribonuclease with anti-tumor activity.";
 RL J. Mol. Biol. 236:1141-1153(1994).
 CC -1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY
 AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR
 IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH
 MOLECULAR WEIGHT RIBOSOMAL RNA.
 CC MOLECULAR WEIGHT: RIBOSOMAL RNA.
 CC DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PDB: 1ONC; 3A-JAN-94.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR Prodom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; 3D-structure.
 FT MOD_RES 1
 FT ACT_SITE 10
 FT ACT_SITE 31
 FT ACT_SITE 97
 FT DISULFID 19
 FT DISULFID 30
 FT DISULFID 48
 FT DISULFID 87
 FT HELIX 3
 FT STRAND 11
 FT STRAND 12
 FT STRAND 19
 FT STRAND 22
 FT TURN 23
 FT TURN 24
 FT TURN 26
 FT TURN 30
 FT STRAND 33
 FT STRAND 38
 FT STRAND 41
 FT STRAND 49
 FT STRAND 50
 FT STRAND 55
 FT STRAND 58
 FT STRAND 63
 FT STRAND 70
 FT TURN 74
 FT TURN 77
 FT STRAND 84
 FT STRAND 86
 FT TURN 91
 FT TURN 92
 FT TURN 93
 FT STRAND 94
 FT STRAND 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 44.8% Score 271.5; DB 1: Length 104;
 Best Local Similarity 48.6%; Pred. No. 7.9e-23;
 Matches 54; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
 QY 2 QNNATEEQKHHIINT-PIICNTIMDNINIVIGGCKRVTETITSSATVKAIGCVI-NMN 59
 DQ 1 QDMLTFQKHITTRWDCCNINSTNLF-----HCKDKNTFYSPRPVKAIGGIASKN 56
 QY 60 VLSTRFQLTCTRTSTTPRCPYSSRTENRYNICVKEENQYPVHAFAGICG 110
 DB 57 VLTSFEFLSDC---NWTSRCKYKLRKSTNKCVCENQAPVHFEVGVSC 104
 RESULT 5
 ANG3_MOUSE STANDARD: PRT: 145 AA.
 ID ANG3_MOUSE
 AC P97802;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
 DE (EF-3).
 GN ANG3 OR ANGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BALB/c;
 RX MEDLINE=97184476; PubMed=9032278;
 RA Fu X., Kamps M.P.;
 RT "Ezra-Fbx1 induces aberrant expression of tissue-specific and
 developmentally regulated genes when expressed in NIH 3T3
 fibroblasts.";
 RL Mol. Cell. Biol. 17:1503-1512(1997).
 CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 HYDROLYZING CELLULAR TRANS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL: U72672; AAC05794.1;
 DR HSP: P10152; IAGI.
 DR MGD: MGI:1201793; Angl.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA: 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR Prodom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal.
 FT SIGNAL 1
 FT CHAIN 24
 FT MOD_RES 25
 FT MOD_RES 25
 FT ACT_SITE 37
 FT ACT_SITE 37
 FT ACT_SITE 64
 FT ACT_SITE 137
 FT DISULFID 50
 FT DISULFID 63
 FT DISULFID 81
 FT DISULFID 130
 SQ SEQUENCE 145 AA; 16696 MW; DE9D3BC92F1D682C CRC64;

Query Match 24.5%; Score 148.5; DB 1; Length 145;
 Best Local Similarity 42.3%; Pred. No. 2.6e-09;
 Matches 33; Conservative 12; Mismatches 24; Indels 9; Gaps 4;

OY 34 CKRYTTFISSATVKAIC-----TGVIMNVLTSTRQNLNCTRTSTTPR-PCYSSRTE 86
 DB 63 CKRYTTFIHDTKNNIKAIKCGKSPYGRNLRISKSPQVYTTCTHKGRSPRPCKRYRASKG 120

OY 87 TETNYICVCKENQYVPHF 104
 DB 121 KDFRYIVACEDGMPVHF 138

RESULT 6
 ANGR_MOUSE STANDARD; PRT: 145 AA.
 AC 064438:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Angiogenin-related protein precursor.
 GN ANGRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Liver;
 RX MEDLINE=96079109; PubMed=6530072;
 RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
 RT "The mouse angiogenin gene family: structures of an angiogenin-related
 RL protein gene and two pseudogenes.";
 CC Genomics 29:200-206(1995).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U22519; AAA91367.1; -;
 DR HSSP: P03950; 1A4Y.
 DR MGD: MGI:104984; Angrp.
 DR InterPro: IPR001427; Rnasea.
 DR Pfam: PF00074; Rnasea; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; Rnasea; 1.
 DR SMART: SM00092; Rnase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Signal: Hydrolyase; Nuclease; Endonuclease.
 FT SIGNAL 1 24
 FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 FT ACT_SITE 37 37 SIMILARITY).
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT DISULFID 50 104 BY SIMILARITY.
 FT DISULFID 63 115 BY SIMILARITY.
 FT DISULFID 81 130 BY SIMILARITY.
 SO SEQUENCE 145 AA; 16612 MW; 29A6EB814429CAD CRC64;

Query Match 23.7%; Score 143.5; DB 1; Length 145;
 Best Local Similarity 42.1%; Pred. No. 9.2e-09;
 Matches 32; Conservative 10; Mismatches 29; Indels 5; Gaps 3;

OY 34 CKRYTTFISSATVKAIC---TGVIMNV-LSTRQNLNCTRTSTTPR-PCYSSRTE 88
 DB 63 CKRYTTFIHDTKNNIKAIKCGKSPYGRNLRISKSPQVYTTCTHKGRSPRPCKRYRASKG 122

OY 89 TNYICVCKENQYVPHF 104
 DB 123 FRIYICGKNGMPVHF 138

RESULT 7
 RNP_BALAC STANDARD; PRT: 124 AA.
 ID RNP_BALAC
 AC P00673:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASE1 OR RN51.
 OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OX NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277855; PubMed=962870;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 RL ribonuclease.";
 CC Biochem. J. 157:317-323(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
 DR HSSP: P00656; 1SRN.
 DR InterPro: IPR001427; Rnasea.
 DR Pfam: PF00074; Rnasea; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; Rnasea; 1.
 DR SMART: SM00092; Rnase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 72 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .); IN 30% OF THE
 FT MOLECULES.
 SO SEQUENCE 124 AA; 14125 MW; F57475455F67E20 CRC64;

Query Match 21.4%; Score 129.5; DB 1; Length 124;
 Best Local Similarity 32.5%; Pred. No. 2.6e-07;
 Matches 38; Conservative 16; Mismatches 40; Indels 23; Gaps 7;

OY 7 FQCKHIT-----NTPICNTIMDNNTIYVGCKRYTTFISSATVKAICGVIMNV 60
 DB 8 FQCKHIT-----NTPICNTIMDNNTIYVGCKRYTTFISSATVKAICGVIMNV 60

OY 61 L-----STTRFQNLNCTRTSTTPR-PCYSSRTEINYICVCKE-NQY-PVHF 104
 DB 64 LCKNGRTNCEVSNSTMTHTDCRQYSGSKYPRCAVKTQSKRHIIIVACEDGMPVPHF 120

RESULT 8
 ANGI_MOUSE STANDARD; PRT: 145 AA.
 ID ANGI_MOUSE
 AC P21570:
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Angiogenin precursor (EC 3.1.27.-).
 GN ANG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.:
 RT "Isolation and sequencing of mouse angiogenin DNA";
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC TISSUE-Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.:
 RT "Characterization and sequencing of rabbit, pig and mouse
 RT angiogenins: discernment of functionally important residues and
 RT regions";
 RL Biochim. Biophys. Acta 1162:177-186(1993).
 CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U22516; AAA91366.1; -;
 DR PIR: A35932; A35932.
 DR HSP: P03950; 1M4Y.
 DR MGD: MGI:86022; Ang.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KM Protein synthesis inhibitor; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 145
 FT MOD_RES 25 25
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 137 137
 FT DISULFID 50 104
 FT DISULFID 63 115
 FT DISULFID 81 130
 FT DISULFID 130 130
 SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
 Query Match 21.4%; Score 129.5; DB 1; Length 145;
 Best Local Similarity 38.2%; Pred. No. 3.1e-07;
 Matches 29; Conservative 12; Mismatches 30; Indels 5; Gaps 3;
 OY 34 CRATVTEPFISSATVKAIC---TGVIMNV-LSTTRPOLNCTCTSTTPR-PCPYSSRTE 88
 Db 63 KREVTNTEHGNKSKIRKICANGSPYHRENLRMSKSPQVTTCKATGSPRCPQYRASAG 122
 OY 89 TNIVCAGENQPYHF 104

Db 123 FRHVIACENGLPYHF 138
 RESULT 9
 RNBR_BOVIN STANDARD; PRT; 167 AA.
 ID RNBR_BOVIN
 AC P39873;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, Brain precursor (EC 3.1.27.-) (BRB).
 GN BRN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92093604; PubMed=1754384;
 RA Sasso M.P., Carsana A., Confalone E., Costi C., Sorrentino S.,
 RA Viola M., Palmieri M., Russo E., Furia A.;
 RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
 RT and its expression in different regions of the brain.";
 RL Nucleic Acids Res. 19:6469-6474(1991).
 RN [2]
 RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
 RC TISSUE-Brain;
 RX MEDLINE=89214015; PubMed=3243767;
 RA Matanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
 RA Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bovine brain.";
 RL J. Biochem. 104:939-945(1988).
 RP SEQUENCE OF 27-167 FROM N.A.
 RX MEDLINE=96139017; PubMed=8587129;
 RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
 RA Vento M.T., Furia A.;
 RT "Molecular evolution of genes encoding ribonucleases in ruminant
 RT species";
 RL J. Mol. Evol. 41:850-858(1995).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X59767; CAA42439.1; -;
 DR EMBL: S81744; AAB36138.1; -;
 DR PIR: S20066; S20066.
 DR PIR: JX0056; JX0056.
 DR HSP: P00656; 2RNS.
 DR GlycoSuiteDB: P39873; -;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 KM Hydrolyase; Nuclease; Endonuclease; glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 167
 FT ACT_SITE 38 38
 FT ACT_SITE 67 67
 FT ACT_SITE 145 145
 FT DISULFID 52 110
 FT DISULFID 66 121
 FT DISULFID 84 136
 FT DISULFID 91 98
 FT DISULFID 91 98

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FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).
FT CARBOHYD 155 155 /FTID-CAR_000005.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 O-LINKED.
SO SEQUENCE 167 AA: 18450 MW: 681CAGC3CC2FC459 CRC64:
Query Match 21.0%; Score 127.5; DB 1; Length 167;
Best Local Similarity 30.6%; Pred. No. 5.9e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 5 ATP00KH-----INPIICNTIMDNNIYVGGCKRYTFTFISSATTVAICTGVIM 58
D 32 AKFR0HMDSSSSSSSNPNYCNOMKKRR-RMTHGRCRKPNTFVHESLDDVKAACS---QK 87
D 59 NVL-----STTRFQNLNTCTRTSTITPRP-CPYSSRTETNYICVCE-NOY-PVHFA 105
D 88 NITCKNGHPCNYGSKSTMSITDCRETGSSKYPNCATKTSOKKITTVACEGNPYPVPHFD 147
OY 106 G 106
D 148 G 148

RESULT 10
RNP_PIG STANDARD: PRT; 124 AA.
AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=96323;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653(1970).
RN [2]
RP REVISION TO 2.
RA Wiereinga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185(1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds.";
RL J. Biol. Chem. 245:654-661(1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP: P00656; NRG.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase: Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84

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FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .).
SO SEQUENCE 124 AA: 13804 MW: 0AC28CDE4111845 CRC64:
Query Match 20.9%; Score 126.5; DB 1; Length 124;
Best Local Similarity 30.7%; Pred. No. 5.5e-07;
Matches 35; Conservative 19; Mismatches 43; Indels 17; Gaps 6;

OY 7 F00KH-----INPIICNTIMDNNIYVGGCKRYTFTFISSATTVAICTGV-INNM 59
D 8 F0R0HMDPSSSSSNPNYCNLMMSRR-NM0GRCKPNTFVHESLADVAACSOINYNCK 66
D 60 VLSTTRFQNLNT-----CTRTSITPRP-CPYSSRTETNYICVCE-NOY-PVHFA 104
D 67 NG0TNCYGSNTMTITDCR0TGRGSSKYPNCATKASQEQKHITVACGNPYPVPHFD 120
OY 106 G 106
D 148 G 148

RESULT 11
RNP_IGUIG STANDARD: PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE-Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic
RT ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP: P00656; ILSO.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase: Nuclease; Endonuclease.
FT MOD_RES 1 80 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 39 91 BY SIMILARITY.
FT ACT_SITE 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SO SEQUENCE 119 AA: 13324 MW: 6072PB5B7B15BD5A CRC64:
Query Match 20.7%; Score 125.5; DB 1; Length 119;
Best Local Similarity 29.6%; Pred. No. 6.8e-07;
Matches 34; Conservative 16; Mismatches 52; Indels 13; Gaps 4;

OY 2 QNATF00KH-----INPIICNTIMDNNIYVGGCKRYTFTFISSATTVAICTGV-INNM 52
D 1 QNATF00KH-----INPIICNTIMDNNIYVGGCKRYTFTFISSATTVAICTGV-INNM 52

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Db 1 QDMS3FONKHIDYPTFSASNPAYCDLMOQR-NLNFCKTNTFVHASPSEIOYCGS 59
 OY 53 --TGVIIMANLSTTRPOLNTCTRTST-PPCPYSSSTETNYICVKNXPVHF 104
 Db 60 GGTHEEDNLDSNESFDLDCKNVGGTAPSSCKYNGTPTKRIACENNOPVHF 114

RESULT 12

RNBR_CAPCA STANDARD: PRT: 151 AA.

AC P79351;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
 OS Capreolus capreolus (roe deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Odocoileinae; Capreolus.
 OX NCBI_TaxID=9858;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278642; Pubmed=9611269.
 RA Beutelman H.J., van der Munnik N., Kleinsdam R.G., Furia A.,
 Beintema J.J.;
 RT "secretory ribonuclease genes and pseudogenes in true ruminants";
 RL Gene 212:259-266(1998).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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CC DR EMBL; Y11673; CAA72371.1;
 CC DR HSSP; P00656; ISRN;
 CC DR InterPro: IPR001427; RNaseA.
 CC Pfam: PF00074; RNaseA; 1.
 CC DR PRINTS; PR00794; RIBONUCLEASE.
 CC DR PRODOM; PD000535; RNaseA; 1.
 CC DR SMART; SM00092; RNase_Pc; 1.
 CC DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 CC FT ACT_SITE 41 41 BY SIMILARITY.
 CC FT DISULFID 23 84 BY SIMILARITY.
 CC FT DISULFID 43 95 BY SIMILARITY.
 CC FT DISULFID 53 110 BY SIMILARITY.
 CC FT DISULFID 63 72 BY SIMILARITY.
 CC FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
 CC FT CARBOHYD 123 129 O-LINKED (BY SIMILARITY).
 CC FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
 CC SQ SEQUENCE 151 AA; 16971 MW; 392DDE6302F006A6 CRC64;

Query Match 20.2% Score 122.5; DB 1; Length 151;
 Best Local Similarity 28.6%; Pred. No. 1.8e-06;
 Matches 34; Conservative 17; Mismatches 45; Indels 23; Gaps 6;

OY 5 ATFOQKHI-----INTPICTIMDNNIYVGGCKRVTFTFIISATVKAICTGYIM 58
 Db 6 AKFRRLHMDSSSSSGNPNYCNOMKRR-KMTHGRCKAPVTFVHESLDYKAVCS---QK 61
 OY 59 NVL-----STTFOLNTCTRTSTPR-PCPYSSSTETNYICVKNQ--YVPHF 104
 Db 62 NITCKHQPCWYOSNSTMTITDCROTGSRYPCAYKTSOKOKIYIVACEGDPYVPHF 120

RESULT 13
 ANG2_BOVIN STANDARD: PRT: 123 AA.
 ID ANG2_BOVIN
 AC P80929;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-2 (EC 3.1.27.-).
 GN ANG2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Serum, and Milk.
 RX MEDLINE=97409980; Pubmed=9266695;
 RA Strzydom D.J., Bond M.D., Vallee B.L.;
 RT "An angiogenic protein from bovine serum and milk -- purification and
 RT primary structure of angiogenin-2";
 RL Eur. J. Biochem. 247:535-544(1997).
 CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC
 CC ACTIVITY. ANGIOGENIN INDICES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC DR HSSP; P10152; IAGI.
 CC DR InterPro: IPR001427; RNaseA.
 CC Pfam: PF00074; RNaseA; 1.
 CC DR PRINTS; PR00794; RIBONUCLEASE.
 CC DR PRODOM; PD000535; RNaseA; 1.
 CC DR SMART; SM00092; RNase_Pc; 1.
 CC DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 CC KW Protein synthesis inhibitor; Glycoprotein.
 CC FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 CC FT ACT_SITE 12 12 BY SIMILARITY.
 CC FT ACT_SITE 39 39 BY SIMILARITY.
 CC FT ACT_SITE 113 113 BY SIMILARITY.
 CC FT DISULFID 25 80 BY SIMILARITY.
 CC FT DISULFID 38 91
 CC FT DISULFID 56 106
 CC FT CARBOHYD 33 33
 CC SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 20.0% Score 121.5; DB 1; Length 123;
 Best Local Similarity 29.6%; Pred. No. 1.9e-06;
 Matches 32; Conservative 19; Mismatches 44; Indels 13; Gaps 5;

OY 7 FQOKHINFTPI-----ICNTIMDNNIYVGGCKRVTFTFIISATVKAICT--TGVIIM 58
 Db 8 FLRKHYPSPPLGHDRCNTMMERR--NMRRPCKDTFTFHGNSDDIRAVCDPRNGEPPR 65
 OY 59 NVLSTTR-FOLNTCTRTSTPR-PCPYSSSTETNYICVKNQ--YVPHF 103
 Db 66 NGLRRSRSPFOVYTCRRHRCGSPRPCTRYAFRANRIVIRCDQDFPIH 113

RESULT 14

RNBR_GIRCA STANDARD: PRT: 141 AA.

AC Q29542; Q29533;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, Brain (EC 3.1.27.-) (BRB).
 GN BRN.
 OS Giraffa camelopardalis (Giraffe).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Girafidae;
 OC Girafidae; Giraffa.
 OX NCBI_TaxID=9894;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RX MEDLINE-96139017; PubMed-8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furla A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species.";
RL J. Mol. Evol. 41:850-858(1995).
RN [2]
RP SEQUENCE OF 31-114 FROM N.A.
RX MEDLINE-93367815; PubMed-8360916;
RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furla A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
RT the genomic DNA of mammalian species.";
RL J. Mol. Evol. 37:29-35(1993).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S81743; AAB36137.1; -
DR EMBL; S65126; AAB27931.1; -
DR HSSP; P00656; 2RNS.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNase_PANCREATIC; 1.
DR Hydrolase; Nuclease; Glycoprotein.
KW Hydrolyase: Nuclease; Glycoprotein.
FT ACT_SITE 41
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MW; 73745EF8079591F CRC64;

Query Match 20.0%; Score 121.5; DB 1; Length 141;
Best Local Similarity 29.8%; Pred. No. 2.2e-06;
Matches 36; Conservative 17; Mismatches 45; Indels 23; Gaps 7;

OY 5 ATFOQKH-----INPIICNTIMDNNIYVGGQCKRVTFITSSATYKAICTGYIM 58
DB 6 AKFRQHMDSGSSSSSNYCNOIMKRR-RMTGRCKPVMTFVHESLADYKAVCS---QK 61
OY 59 NVL-----STFRQINTCTRTSITPRP-CPYSSRTETNYCKE-NOY-PVHFA 105
DB 62 NITCKNGQPCNOYNSNTMNTDCKRETGSSKYPNCAYTSOKKITVACGPNPVPHFD 121

OY 106 G 106
DB 122 G 122

RESULT 15
RNRB_AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, Brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Axis.

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OX NCBI_TaxID=57737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96278642; PubMed-9611269;
RA Breukelman H.J., van der Munnik N., Kleinedam R.G., Furla A.,
RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC
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DR EMBL; Y11670; CAA72368.1; -
DR HSSP; P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNase_PANCREATIC; 1.
DR Hydrolase; Nuclease; Glycoprotein.
KW Hydrolyase: Nuclease; Glycoprotein.
FT ACT_SITE 41
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; 16819 MW; E93F3757FC3B233 CRC64;

Query Match 20.0%; Score 121.5; DB 1; Length 151;
Best Local Similarity 29.8%; Pred. No. 2.4e-06;
Matches 36; Conservative 17; Mismatches 45; Indels 23; Gaps 7;

OY 5 ATFOQKH-----INPIICNTIMDNNIYVGGQCKRVTFITSSATYKAICTGYIM 58
DB 6 AKFRQHMDSGSSSSSNYCNOIMKRR-RMTGRCKPVMTFVHESLADYKAVCS---QK 61
OY 59 NVL-----STFRQINTCTRTSITPRP-CPYSSRTETNYCKE-NOY-PVHFA 105
DB 62 NITCKNGQPCNOYNSNTMNTDCKRETGSSKYPNCAYTSOKKITVACGPNPVPHFD 121

OY 106 G 106
DB 122 G 122

Search completed: June 25, 2003, 14:50:06
Job time : 6.76512 secs

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